

SEQUENCE LISTING

<110> Alitalo, Kari  
Joukov, Vladimir

<120> VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN  
AND GENE, MUTANTS THEREOF, AND USES THEREOF

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<150> 09/355,700  
<151> 1999-11-05

<150> PCT/US98/01973  
<151> 1998-02-02

<150> 08/795,430  
<151> 1997-02-05

<150> PCT/FI96/00427  
<151> 1996-08-01

<150> 08/671,573  
<151> 1996-06-28

<150> 08/601,132  
<151> 1996-02-14

<150> 08/585,895  
<151> 1996-01-12

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<150> 08/340,011  
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<170> PatentIn Ver. 2.0

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<220>  
<223> Human Flt4 cDNA (3' end-long form)

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His Arg Gln Glu Ser Gly Phe Arg  
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Leu Lys

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<213> Artificial Sequence

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55 60 65  
gat gaa ctc atg act gta ctc tac cca gaa tat tgg aaa atg tac aag 597  
Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys  
70 75 80  
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85 90 95  
ctc aac tca agg aca gaa gag act ata aaa ttt gct gca gca cat tat 693  
Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr  
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tgc atg cca cgg gag gtg tgt ata gat gtg ggg aag gag ttt gga gtc 789  
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195 200 205 210

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215 220 225

cgt tcc ctg cca gca aca cta cca cag tgt cag gca gcg aac aag acc 1077  
Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr  
230 235 240

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245 250 255

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275 280 285 290

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295 300 305

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His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys  
310 315 320

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375 380 385

cca tgt acg aac cgc cag aag gct tgt gag cca gga ttt tca tat agt 1557  
Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser  
390 395 400

gaa gaa gtg tgt cgt tgt gtc cct tca tat tgg aaa aga cca caa atg 1605  
Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro Gln Met  
405 410 415

1658  
agc taagattgt a ctgtttcca gttcatcgat tttctattat ggaaaactgt  
Ser

1718  
gttgccacag tagaactgtc tgtgaacaga gagacccttg tgggtccatg ctaacaaaga  
caaaagtctg tcttcctga accatgtgga taactttaca gaaatggact ggagctcatc 1778

1838  
tgcaaaaggc ctcttgtaaa gactggttt ctgccaatga ccaaacagcc aagattttcc  
tcttgatt tctttaaaag aatgactata taatttattt ccactaaaaa tattgtttct 1898

1958  
gcattcattt ttatagcaac aacaattggt aaaactcact gtgatcaata ttttatatc  
atgcaaaaata tggtaaaat aaaatgaaaa ttgtattat 1997

<210> 8  
<211> 419  
<212> PRT  
<213> Homo sapiens

<400> 8  
Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala  
1 5 10 15  
Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe  
20 25 30  
Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala  
35 40 45  
Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser  
50 55 60  
Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met  
65 70 75 80  
Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln  
85 90 95  
Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala  
100 105 110  
His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys  
115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe  
130 135 140  
Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr  
145 150 155 160  
Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr  
165 170 175  
Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu  
180 185 190  
Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser  
195 200 205  
Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile  
210 215 220  
Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn  
225 230 235 240  
Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys  
245 250 255  
Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser  
260 265 270  
Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu  
275 280 285  
Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys  
290 295 300  
Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys  
305 310 315 320  
Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu  
325 330 335  
Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro  
340 345 350  
Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys  
355 360 365  
Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr  
370 375 380  
Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser  
385 390 395 400  
Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro  
405 410 415  
Gln Met Ser

<210> 9  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<220>  
<223> VEGF-C peptide "PAM126"

<400> 9  
Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu  
1 5 10 15

Lys

<210> 10  
<211> 1836  
<212> DNA  
<213> Murine

<220>  
<221> CDS  
<222> (168)..(1412)

<220>  
<223> cDNA encoding murine VEGF-C precursor

<400> 10  
gcggccgcgt cgacgcaaaa gttgcgagcc gccgagtcgg gggagacgct cgcccaagggg 60  
ggtccccggg aggaaaccac gggacagggg ccaggagagg acctcagcct cacgccccag 120  
cctgcgccag ccaacggacc ggcctccctg ctcccggtcc atccacc atg cac ttg 176  
Met His Leu  
1

224  
ctg tgc ttc ttg tct ctg gcg tgt tcc ctg ctc gcc gct gcg ctg atc  
Leu Cys Phe Leu Ser Leu Ala Cys Ser Leu Leu Ala Ala Ala Leu Ile  
5 10 15

272  
ccc agt ccg cgc gag gcg ccc gcc acc gtc gcc ttc gag tcg gga  
Pro Ser Pro Arg Glu Ala Pro Ala Thr Val Ala Ala Phe Glu Ser Gly  
20 25 30 35

320  
ctg ggc ttc tcg gaa gcg gag ccc gac ggg ggc gag gtc aag gct ttt  
Leu Gly Phe Ser Glu Ala Glu Pro Asp Gly Gly Glu Val Lys Ala Phe  
40 45 50

gaa ggc aaa gac ctg gag gag cag ttg cgg tct gtg tcc agc gta gat 368  
Glu Gly Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val Asp  
55 60 65

gag ctg atg tct gtc ctg tac cca gac tac tgg aaa atg tac aag tgc 416  
Glu Leu Met Ser Val Leu Tyr Pro Asp Tyr Trp Lys Met Tyr Lys Cys  
70 75 80

cag ctg cgg aaa ggc ggc tgg cag cag ccc acc ctc aat acc agg aca 464  
Gln Leu Arg Lys Gly Gly Trp Gln Gln Pro Thr Leu Asn Thr Arg Thr  
85 90 95

ggg gac agt gta aaa ttt gct gct gca cat tat aac aca gag atc ctg 512  
Gly Asp Ser Val Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu  
100 105 110 115

aaa agt att gat aat gag tgg aga aag act caa tgc atg cca cgt gag 560  
Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu  
120 125 130

gtg tgt ata gat gtg ggg aag gag ttt gga gca gcc aca aac acc ttc 608  
Val Cys Ile Asp Val Gly Lys Glu Phe Gly Ala Ala Thr Asn Thr Phe  
135 140 145

ttt aaa cct cca tgt gtg tcc gtc tac aga tgt ggg ggt tgc tgc aac 656  
Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn  
150 155 160

agc gag ggg ctg cag tgc atg aac acc agc aca ggt tac ctc agc aag 704  
Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Gly Tyr Leu Ser Lys  
165 170 175

acg ttg ttt gaa att aca gtg cct ctc tca caa ggc ccc aaa cca gtc 752  
Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro Lys Pro Val  
180 185 190 195

aca atc agt ttt gcc aat cac act tcc tgc cgg tgc atg tct aaa ctg 800  
Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu  
200 205 210

gat gtt tac aga caa gtt cat tca att att aga cgt tct ctg cca gca 848  
Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser Leu Pro Ala  
215 220 225

aca tta cca cag tgt cag gca gct aac aag aca tgt cca aca aac tat 896  
Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro Thr Asn Tyr  
230 235 240

gtg tgg aat aac tac atg tgc cga tgc ctg gct cag cag gat ttt atc 944  
Val Trp Asn Asn Tyr Met Cys Arg Cys Leu Ala Gln Gln Asp Phe Ile  
245 250 255

ttt tat tca aat gtt gaa gat gac tca acc aat gga ttc cat gat gtc 992  
Phe Tyr Ser Asn Val Glu Asp Asp Ser Thr Asn Gly Phe His Asp Val  
260 265 270 275

tgt gga ccc aac aag gag ctg gat gaa gac acc tgt cag tgc tgc 1040  
Cys Gly Pro Asn Lys Glu Leu Asp Glu Asp Thr Cys Gln Cys Val Cys  
280 285 290

aag ggg ggg ctt cgg cca tct agt tgt gga ccc cac aaa gaa cta gat 1088  
Lys Gly Gly Leu Arg Pro Ser Ser Cys Gly Pro His Lys Glu Leu Asp  
295 300 305

aga gac tca tgt cag tgt gtc tgt aaa aac aaa ctt ttc cct aat tca 1136  
Arg Asp Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe Pro Asn Ser  
310 315 320

tgt gga gcc aac agg gaa ttt gat gag aat aca tgt cag tgt gta tgt 1184  
Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln Cys Val Cys  
325 330 335

aaa aga acg tgt cca aga aat cag ccc ctg aat cct ggg aaa tgt gcc 1232  
Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala  
340 345 350 355

tgt gaa tgt aca gaa aac aca cag aag tgc ttc ctt aaa ggg aag aag 1280  
Cys Glu Cys Thr Glu Asn Thr Gln Lys Cys Phe Leu Lys Gly Lys Lys  
360 365 370

ttc cac cat caa aca tgc agt tgt tac aga aga ccg tgt gcg aat cga 1328  
Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys Ala Asn Arg  
375 380 385

ctg aag cat tgt gat cca gga ctg tcc ttt agt gaa gaa gta tgc cgc 1376  
Leu Lys His Cys Asp Pro Gly Leu Ser Phe Ser Glu Glu Val Cys Arg  
390 395 400

tgt gtc cca tcg tat tgg aaa agg cca cat ctg aac taagatcata 1422  
Cys Val Pro Ser Tyr Trp Lys Arg Pro His Leu Asn  
405 410 415

ccagtttca gtcagtcaca gtcatttact ctcttgaaga ctgttggAAC agcacttagc 1482  
actgtctatg cacagaaaga ctctgtggga ccacatggta acagaggccc aagtctgtgt 1542  
ttattgaacc atgtggatta ctgcggaga ggactggcac tcatgtgcaa aaaaaacctc 1602  
ttcaaaagact ggtttctgc cagggaccag acagctgagg ttttctctt gtgatttaaa 1662  
aaaagaatga ctatataatt tatttccact aaaaatattg ttccctgcatt cattttata 1722  
gcaataacaa ttggtaaagc tcactgtgat cagtatttt ataacatgca aaactatgtt 1782  
taaaataaaa tgaaaattgt attataaaaa aaaaaaaaaa aaaaaaaaaa gctt 1836

<210> 11  
<211> 415  
<212> PRT  
<213> Murine

<400> 11  
Met His Leu Leu Cys Phe Leu Ser Leu Ala Cys Ser Leu Leu Ala Ala  
1 5 10 15  
Ala Leu Ile Pro Ser Pro Arg Glu Ala Pro Ala Thr Val Ala Ala Phe  
20 25 30  
Glu Ser Gly Leu Gly Phe Ser Glu Ala Glu Pro Asp Gly Gly Glu Val  
35 40 45  
Lys Ala Phe Glu Gly Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser  
50 55 60  
Ser Val Asp Glu Leu Met Ser Val Leu Tyr Pro Asp Tyr Trp Lys Met  
65 70 75 80  
Tyr Lys Cys Gln Leu Arg Lys Gly Trp Gln Gln Pro Thr Leu Asn  
85 90 95  
Thr Arg Thr Gly Asp Ser Val Lys Phe Ala Ala Ala His Tyr Asn Thr  
100 105 110  
Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met  
115 120 125  
Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Ala Ala Thr  
130 135 140  
Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly  
145 150 155 160  
Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Gly Tyr  
165 170 175  
Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro  
180 185 190  
Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met  
195 200 205  
Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser  
210 215 220  
Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro  
225 230 235 240  
Thr Asn Tyr Val Trp Asn Asn Tyr Met Cys Arg Cys Leu Ala Gln Gln  
245 250 255  
Asp Phe Ile Phe Tyr Ser Asn Val Glu Asp Asp Ser Thr Asn Gly Phe  
260 265 270  
His Asp Val Cys Gly Pro Asn Lys Glu Leu Asp Glu Asp Thr Cys Gln  
275 280 285

Cys Val Cys Lys Gly Gly Leu Arg Pro Ser Ser Cys Gly Pro His Lys  
290 295 300  
Glu Leu Asp Arg Asp Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe  
305 310 315 320  
Pro Asn Ser Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln  
325 330 335  
Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly  
340 345 350  
Lys Cys Ala Cys Glu Cys Thr Glu Asn Thr Gln Lys Cys Phe Leu Lys  
355 360 365  
Gly Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys  
370 375 380  
Ala Asn Arg Leu Lys His Cys Asp Pro Gly Leu Ser Phe Ser Glu Glu  
385 390 395 400  
Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro His Leu Asn  
405 410 415

<210> 12

<211> 1741

<212> DNA

<213> Quail

<220>

<221> CDS

<222> (453) .. (1706)

<220>

<223> Quail VEGF-C cDNA

<400> 12

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gcgagccggcc actgggtcct gcttcctcc ttccctctccc tccctctcct cctccttctc 120  
tctgcgttt ccaccgctcc cgagcgagcg cacgctcgga tgcgggttt cctgggtgggt 180  
tttttacctg gcaaagtccg gataacttcg gtgagaattt gcaaagaggg tgggagctcc 240  
cctgcaggcg tctggagct gctggccgcg tcgcacatcttc tccatcccgc ggattttact 300  
gccttggata ttgcgagggg agggaggggg gtgaggacag caaaaagaaa ggggtggggg 360  
gggggagaga aaaggaaaag aaggagccctc ggaattgtgc ccgcattcct gcgcgtgcccc 420  
gcggcccccc tccgcgtctgc catctccgca ca atg cac ttg ctg gag atg ctc 473  
Met His Leu Leu Glu Met Leu

tcc ctg ggc tgc tgc ctc gct gct ggc gcc gtg ctc ctc gga ccc cgg 521  
Ser Leu Gly Cys Cys Leu Ala Ala Gly Ala Val Leu Leu Gly Pro Arg  
10 15 20

cag ccg ccc gtc gcc gcc tac gag tcc ggg cac ggc tac tac gag 569  
Gln Pro Pro Val Ala Ala Tyr Glu Ser Gly His Gly Tyr Tyr Glu  
25 30 35

gag gag ccc ggt gcc ggg gaa ccc aag gct cat gca agc aaa gac ctg 617  
Glu Glu Pro Gly Ala Gly Glu Pro Lys Ala His Ala Ser Lys Asp Leu  
40 45 50 55

gaa gag cag ttg cga tct gtg tcc agt gtg gat gaa ctc atg aca gta 665  
Glu Glu Gln Leu Arg Ser Val Ser Val Asp Glu Leu Met Thr Val  
60 65 70

ctt tac cca gaa tac tgg aaa atg ttc aaa tgt cag ttg agg aaa gga 713  
Leu Tyr Pro Glu Tyr Trp Lys Met Phe Lys Cys Gln Leu Arg Lys Gly  
75 80 85

ggt tgg caa cac aac agg gaa cac tcc agc tct gat aca aga tca gat 761  
Gly Trp Gln His Asn Arg Glu His Ser Ser Asp Thr Arg Ser Asp  
90 95 100

gat tca ttg aaa ttt gcc gca gca cat tat aat gca gag atc ctg aaa 809  
Asp Ser Leu Lys Phe Ala Ala Ala His Tyr Asn Ala Glu Ile Leu Lys  
105 110 115

agt att gat act gaa tgg aga aaa acc cag ggc atg cca cgt gaa gtg 857  
Ser Ile Asp Thr Glu Trp Arg Lys Thr Gln Gly Met Pro Arg Glu Val  
120 125 130 135

tgt gtg gat ttg ggg aaa gag ttt gga gca act aca aac acc ttc ttt 905  
Cys Val Asp Leu Gly Lys Glu Phe Gly Ala Thr Thr Asn Thr Phe Phe  
140 145 150

aaa ccc ccg tgt gta tcc atc tac aga tgt gga ggt tgc tgc aat agt 953  
Lys Pro Pro Cys Val Ser Ile Tyr Arg Cys Gly Cys Cys Asn Ser  
155 160 165

gaa gga ctc cag tgt aat atc agc aca aat tac atc agc aag aca 1001  
Glu Gly Leu Gln Cys Met Asn Ile Ser Thr Asn Tyr Ile Ser Lys Thr  
170 175 180

ttg ttt gag att aca gtg cct ctc tct cat ggc ccc aaa cct gta aca 1049  
Leu Phe Glu Ile Thr Val Pro Leu Ser His Gly Pro Lys Pro Val Thr  
185 190 195

gtc agt ttt gcc aat cac acg tcc tgc cga tgc atg tct aag ttg gat 1097  
Val Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu Asp  
200 205 210 215

gtt tac aga caa gtt cat tct atc ata aga cgt tcc ttg cca gca aca 1145  
Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser Leu Pro Ala Thr  
220 225 230

caa act cag tgt cat gtg gca aac aag acc tgt cca aaa aat cat gtc 1193  
Gln Thr Gln Cys His Val Ala Asn Lys Thr Cys Pro Lys Asn His Val  
235 240 245

tgg aat aat cag att tgc aga tgc tta gca cag cac gat ttt ggt ttc 1241  
Trp Asn Asn Gln Ile Cys Arg Cys Leu Ala Gln His Asp Phe Gly Phe  
250 255 260

tct tct cac ctt gga gat tct gac aca tct gaa gga ttc cat att tgt 1289  
Ser Ser His Leu Gly Asp Ser Asp Thr Ser Glu Gly Phe His Ile Cys  
265 270 275

ggg ccc aac aaa gag ctg gat gaa gaa acc tgt caa tgc gtc tgc aaa 1337  
Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Lys  
280 285 290 295

gga ggt gtg cgg ccc ata agc tgt ggc cct cac aaa gaa cta gac agg 1385  
Gly Gly Val Arg Pro Ile Ser Cys Gly Pro His Lys Glu Leu Asp Arg  
300 305 310

gca tca tgt cag tgc atg tgc aaa aac aaa ctg ctc ccc agt tcc tgt 1433  
Ala Ser Cys Gln Cys Met Cys Lys Asn Lys Leu Leu Pro Ser Ser Cys  
315 320 325

ggg cct aac aaa gaa ttt gat gaa gaa aag tgc cag tgt gta tgt aaa 1481  
Gly Pro Asn Lys Glu Phe Asp Glu Glu Lys Cys Gln Cys Val Cys Lys  
330 335 340

aag acc tgt ccc aaa cat cat cca cta aat cct gca aaa tgc atc tgc 1529  
Lys Thr Cys Pro Lys His His Pro Leu Asn Pro Ala Lys Cys Ile Cys  
345 350 355

gaa tgt aca gaa tct ccc aat aaa tgt ttc tta aaa gga aaa aga ttt 1577  
Glu Cys Thr Glu Ser Pro Asn Lys Cys Phe Leu Lys Gly Lys Arg Phe  
360 365 370 375

cat cac cag aca tgc agt tgt tac aga cca cca tgt aca gtc cga acg 1625  
His His Gln Thr Cys Ser Cys Tyr Arg Pro Pro Cys Thr Val Arg Thr  
380 385 390

aaa cgc tgt gat gct gga ttt ctg tta gct gaa gaa gtg tgc cgc tgt 1673  
Lys Arg Cys Asp Ala Gly Phe Leu Leu Ala Glu Glu Val Cys Arg Cys  
395 400 405

gta cgc aca tct tgg aaa aga cca ctt atg aat taagcgaaga aagcactact 1726  
Val Arg Thr Ser Trp Lys Arg Pro Leu Met Asn  
410 415

cgctatatag tgtcg 1741

<210> 13  
<211> 418  
<212> PRT  
<213> Quail

<400> 13  
Met His Leu Leu Glu Met Leu Ser Leu Gly Cys Cys Leu Ala Ala Gly  
1 5 10 15  
Ala Val Leu Leu Gly Pro Arg Gln Pro Pro Val Ala Ala Ala Tyr Glu  
20 25 30  
Ser Gly His Gly Tyr Tyr Glu Glu Glu Pro Gly Ala Gly Glu Pro Lys  
35 40 45  
Ala His Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser  
50 55 60  
Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Phe  
65 70 75 80  
Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu His Ser  
85 90 95  
Ser Ser Asp Thr Arg Ser Asp Asp Ser Leu Lys Phe Ala Ala Ala His  
100 105 110  
Tyr Asn Ala Glu Ile Leu Lys Ser Ile Asp Thr Glu Trp Arg Lys Thr  
115 120 125  
Gln Gly Met Pro Arg Glu Val Cys Val Asp Leu Gly Lys Glu Phe Gly  
130 135 140  
Ala Thr Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Ile Tyr Arg  
145 150 155 160  
Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Ile Ser  
165 170 175  
Thr Asn Tyr Ile Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser  
180 185 190  
His Gly Pro Lys Pro Val Thr Val Ser Phe Ala Asn His Thr Ser Cys  
195 200 205  
Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile  
210 215 220  
Arg Arg Ser Leu Pro Ala Thr Gln Thr Gln Cys His Val Ala Asn Lys  
225 230 235 240  
Thr Cys Pro Lys Asn His Val Trp Asn Asn Gln Ile Cys Arg Cys Leu  
245 250 255  
Ala Gln His Asp Phe Gly Phe Ser Ser His Leu Gly Asp Ser Asp Thr  
260 265 270  
Ser Glu Gly Phe His Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu  
275 280 285

Thr Cys Gln Cys Val Cys Lys Gly Gly Val Arg Pro Ile Ser Cys Gly  
290 295 300  
Pro His Lys Glu Leu Asp Arg Ala Ser Cys Gln Cys Met Cys Lys Asn  
305 310 315 320  
Lys Leu Leu Pro Ser Ser Cys Gly Pro Asn Lys Glu Phe Asp Glu Glu  
325 330 335  
Lys Cys Gln Cys Val Cys Lys Thr Cys Pro Lys His His Pro Leu  
340 345 350  
Asn Pro Ala Lys Cys Ile Cys Glu Cys Thr Glu Ser Pro Asn Lys Cys  
355 360 365  
Phe Leu Lys Gly Lys Arg Phe His His Gln Thr Cys Ser Cys Tyr Arg  
370 375 380  
Pro Pro Cys Thr Val Arg Thr Lys Arg Cys Asp Ala Gly Phe Leu Leu  
385 390 395 400  
Ala Glu Glu Val Cys Arg Cys Val Arg Thr Ser Trp Lys Arg Pro Leu  
405 410 415

Met Asn

<210> 14  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<220>  
<223> IgG-Kappa sequence

<400> 14  
Ala Val Val Met Thr Gln Thr Pro Ala Ser  
1 5 10

<210> 15  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 15  
tctcttctgt gcttgagttg ag

<210> 16  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 16  
tctcttctgt ccctgagttg ag

22

<210> 17  
<211> 65  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 17  
tgtgctgcag caaattttat agtctttctt gtggcggcgg cggcggcggg cgcctcgcg 60

65

ggacc

<210> 18  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 18  
ctggcaggga actgctaata atggaatgaa

30

<210> 19  
<211> 84  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 19  
gggctccgca tccgagaggt cgagtccgga ctcgtgatgg tgatggatgg gggcggcggc 60

84

ggcggcgggc gcctcgcgag gacc

<210> 20  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 20 31  
gtattataat gtcctccacc aaattttata g

<210> 21  
<211> 93  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 21 93  
gttcgctgcc tgacactgtg gtagtgttgc tggcggccgc tagtgatggt gatggtgatg 60  
aataatggaa tgaacttgtc tgtaaacatc cag

<210> 22  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 22 17  
catgtacgaa ccgccag

<210> 23  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 23 20  
aatgaccaga gagaggcag

<210> 24  
<211> 24

<212> DNA  
<213> Homo sapiens

<400> 24  
ggcgaggcca cggttaggtct gcgt

24

<210> 25  
<211> 24  
<212> DNA  
<213> Homo sapiens

<400> 25  
tttctttgac aggcttatgc aagc

24

<210> 26  
<211> 24  
<212> DNA  
<213> Homo sapiens

<400> 26  
gagatcttga aaagtaagta tggg

24

<210> 27  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 27  
atgacttgac aggtattgtat aat

23

<210> 28  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 28  
ctcagcaaga cggtgggtat tgt

23

<210> 29  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 29  
cccttcttg tagttatgg aaatt

25

<210> 30  
<211> 27  
<212> DNA

<213> Homo sapiens

<400> 30  
acactaccac agtgagtatg aattaaa

27

<210> 31  
<211> 24  
<212> DNA  
<213> Homo sapiens

<400> 31  
ttcttccaaa ggtgtcaggc agcg

24

<210> 32  
<211> 21  
<212> DNA  
<213> Homo sapiens

<400> 32  
gctggagatg gtagcagaat g

21

<210> 33  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 33  
ctatttgtct agactcaaca gat

23

<210> 34  
<211> 22  
<212> DNA  
<213> Homo sapiens

<400> 34  
caaacatgca ggtaagagat cc

22

<210> 35  
<211> 24  
<212> DNA  
<213> Homo sapiens

<400> 35  
tgttctccata gctgttacag acgg

24

<210> 36  
<211> 24  
<212> DNA  
<213> Murine

<400> 36  
ggcgagggtca aggttaggtgc aagg

24

<210> 37  
<211> 26  
<212> DNA  
<213> Murine

<400> 37  
attgtctttg acaggctttt tgaagg

26

<210> 38  
<211> 21  
<212> DNA  
<213> Murine

<400> 38  
gagatcctga aaagtaagta g

21

<210> 39  
<211> 24  
<212> DNA  
<213> Murine

<400> 39  
tgtgactcga caggtattga taat

24

<210> 40  
<211> 20  
<212> DNA  
<213> Murine

<400> 40  
ctcagcaaga cggtaggtat

20

<210> 41  
<211> 25  
<212> DNA  
<213> Murine

<400> 41  
ttgtcccttg tagttgtttg aaatt

25

<210> 42  
<211> 20  
<212> DNA  
<213> Murine

<400> 42

acattaccac agtgagtatg

<210> 43  
<211> 26  
<212> DNA  
<213> Murine

<400> 43  
gtctcccaa aagggtgtcag gcagct

26

<210> 44  
<211> 23  
<212> DNA  
<213> Murine

<400> 44  
aatgttgaag atggtaagta aaa

23

<210> 45  
<211> 16  
<212> DNA  
<213> Murine

<400> 45  
tctagactca accaat

16

<210> 46  
<211> 22  
<212> DNA  
<213> Murine

<400> 46  
caaacatgca ggtaaggagt gt

22

<210> 47  
<211> 24  
<212> DNA  
<213> Murine

<400> 47  
ttttcccta gttgttacag aaga

24

<210> 48  
<211> 2991  
<212> DNA  
<213> Homo sapiens

<220>  
<223> Genomic DNA - Sequence upstream of VEGF-C coding

sequence

<400> 48  
gttttaagta gagacggggt ttcaccaacg gttgaaaata tttatcatgg tctccctaag 60  
atggacggtg ttagcttagga tggctcgat ctccgtacccatgatccac ccgcctcg 120  
ctcccaaagt gctgggatta caggcgtgag ccaccgtgc cgaccaacct taagacaaac 180  
aactactgca tgattgttt tggagacctt ttttttattt aaataaattt ttgccagcat 240  
tttctgactc aaagtatagc agcaggaaga taacactttt gtgagaaaaa agtttgaata 300  
cagcttactg ctgtatattaa atgaaacagt agttaatatg atattaatat attttgata 360  
tattttgagt ttgttgattt tccagtc tccaccgtgct aggcctgtgg gtgttgaaa 420  
tgcctgtgtt tctcaatttt gtttgctat tagaattcctg atgtccaagc cttactccag 480  
ttagaccagt taagccagaa aggcagaagg tgtactcaag catctgtttt ttcaaaatct 540  
ccttttgc tgccttgc aatcaaagt tagaattcatt gtaatagcaa atggttgaat 600  
ggaaactcca ccttctattt aaatcctacc ccagtctgcc cttagctgtt ctctttcac 660  
agatctatca atgtctgaag ataactatgg caggctgatc aaatatgcat agagcagggaa 720  
gacagcaaga gagtgataca ctgaccatgt tccaaatcac aaaacatctc aacaggctag 780  
atcatggacc gagtctgatg ggttggaaatt tcataaagat acataaaaaaa gcatcttgaa 840  
tacagtaaac ttaactccac aaatacaggg gaatttagac gtgactaagt agcagtacat 900  
atgaaaaattt attgaggaat tttgttgact ttaaggtag tttgttgactaa cactgtgatt 960  
tggctgccag aaaataaact caatccaagg ctgtatcaac aaaggcatac tgtccattct 1020  
gcatgctcat tacagcacta agtaccgagc catgttctca accgcatact tcatgaacat 1080  
ggaaagctaa cagtatggtt aaggggggaa actggaaactg tcattttggg gaataaaagg 1140  
gatatttagc caggagtaaa gtttagcttag ggagaccatg ataaatattt tcaaaatattt 1200  
tgaaggactc agttgtggaa gtgagattt atttatttgtaaaactcca ggagtcaaaa 1260  
gcaatagaga gatagaagga aatgctttc agcagtgttg ctcataata aaggagtgaa 1320  
acagccacac agaatggaaag gttccctgtc cttttagata tttaaggcattt caagtaattt 1380  
atgggtgagg agtttcaat ctagagttga accagataag aaagtctttt cttccggtaa 1440  
gatattatgg acctataaca tctgtgtact taaaagttaga ttggggagtga aaggcagact 1500  
tttgatgttc tgtacactgt tgaaaccct tagcgtggtc ctctgttaacc tgctcaccc 1560

gccccaaagga ggcagctagc caatgccacc agcccaacgg aaaccccaagt gctttccaa 1620  
tggggaaatg cagtcacttt tctttggatg ctacacatcc tttctggaat atgtctcaca 1680  
cacatctctc tttatcaccc ccttttcaa gtaaaccaac ttcttgaga agctgacaat 1740  
gtgtctctt actctccacg aagattctgg cccttctttt cacctgtcag aagtttagga 1800  
ttccaaaggg atcattagca tccatccaa cagcctgcac tgcatcctga gaactgcgg 1860  
tcttggatca tcaggcaact ttcaactaca cagaccaagg gagagagggg acccctccga 1920  
ggtcccatag gttctctga catagtatg accttttcc aaacttttag cagggcgctg 1980  
ggggccaggg gtgcgggagg gaggacaaga actcgggagt ggccgaggat aaagcggggg 2040  
ctccctccac cccacgggtgc ccagttctc cccgctgcac gtggccagg gtggcgcac 2100  
cacctctaaa gccggccccg ccaaccgcac gccccgggac tgaacttgcc cctccggccg 2160  
cccgctcccc gcaggggaca ggggcggggg gggagagatc cagagggggg ctgggggagg 2220  
tggggccgccc ggggaggagg cgagggaaac ggggagctcc agggagacgg cttccgaggg 2280  
agagtgagag gggagggcag cccgggctcg gcacgctccc tccctggcc gctttctctc 2340  
acataagcgc aggcagaggg cgctcagtc atgcctgcac cctgcggccg cggccggccg 2400  
cgccgcgcgt cagccggcg cgctctggag gatcctgcgc cgccgcgcgt ccggccccc 2460  
ccgcccgcag ccgccccggc ggccctcctc ccgcggccgg caccgcccgc agcgcccc 2520  
ccgcagcgcc cgcgccccgg ctcctctcac ttctgggaag gggagggagg agggggacga 2580  
gggctctggc gggtttggag gggctgaaca tcgcggggtg ttctgggtgc ccccgcccc 2640  
cctctccaaa aagctacacc gacgcggacc gcggcgccgt ctcctctgc ctcgcgttca 2700  
cctcgccggc tccgaatgcg gggagctcg atgtccgggt tcctgtgagg cttttacctg 2760  
acacccggccg ctttccccg gcactggctg ggagggcgcc ctgcaaagtt gggAACGCGG 2820  
agccccggac ccgctcccgcc cgccctccggc tcgcggccgg ggggtcgccg ggaggagccc 2880  
gggggagagg gaccaggagg ggccccggc ctcgcagggg cgcccgccccc cccacccctg 2940  
cccccgccag cggaccggtc ccccaccccc ggtccttcca ccatgcactt g 2991

<210> 49

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide

<400> 49  
cacggcttat gcaagcaaag

20

<210> 50  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 50  
aacacagttt tccataatag

20

<210> 51  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 51  
Leu Ser Lys Thr Val Ser Gly Ser Glu Gln Asp Leu Pro His Glu Leu  
1 5 10 15

His Val Glu

<210> 52  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide

<400> 52  
gacggacaca gatggaggtt taaag

25

<210> 53  
<211> 196  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Human PDGF-A

<400> 53  
Met Arg Thr Leu Ala Cys Leu Leu Leu Gly Cys Gly Tyr Leu Ala  
1 5 10 15  
His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg  
20 25 30  
Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu  
35 40 45  
Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg  
50 55 60  
Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu  
65 70 75 80  
Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys  
85 90 95  
Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro  
100 105 110  
Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg  
115 120 125  
Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg  
130 135 140  
Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys  
145 150 155 160  
Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu  
165 170 175  
Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp  
180 185 190  
Thr Asp Val Arg  
195

<210> 54  
<211> 241  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Human PDGF-B

<400> 54  
Met Asn Arg Cys Trp Ala Leu Phe Leu Ser Leu Cys Cys Tyr Leu Arg  
1 5 10 15  
Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met  
20 25 30

Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu  
35 40 45  
His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met  
50 55 60  
Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg  
65 70 75 80  
Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu  
85 90 95  
Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp  
100 105 110  
Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln  
115 120 125  
Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr  
130 135 140  
Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg  
145 150 155 160  
Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu  
165 170 175  
Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser  
180 185 190  
Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val  
195 200 205  
Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg  
210 215 220  
Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly  
225 230 235 240  
Ala

<210> 55  
<211> 149  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Human PIGF

<400> 55  
Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly  
5 10 15

Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly  
20 25 30

Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly  
35 40 45

Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu  
50 55 60

Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu  
65 70 75 80

Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro  
85 90 95

Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly  
100 105 110

Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys  
115 120 125

Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Cys Gly Asp  
130 135 140

Ala Val Pro Arg Arg  
145

<210> 56  
<211> 191  
<212> PRT  
<213> Homo sapiens

<220>  
<223> VEGF165 precursor

<400> 56  
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu  
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
100 105 110  
Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
115 120 125  
Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly  
130 135 140  
Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr  
145 150 155 160  
Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln  
165 170 175  
Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg  
180 185 190

<210> 57  
<211> 188  
<212> PRT  
<213> Homo sapiens

<220>  
<223> VEGF-B167

<400> 57  
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu  
1 5 10 15  
Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
20 25 30  
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
35 40 45  
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
50 55 60  
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
65 70 75 80  
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
85 90 95  
Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
100 105 110  
Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
115 120 125  
Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg  
130 135 140

Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg  
145 150 155 160

Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu  
165 170 175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg  
180 185

<210> 58

<211> 419

<212> PRT

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: VEGF-C delta Cys156 mutant

<220>  
<223> At position 156, "Xaa" can be anything other than cysteine or can be  
nothing

<400> 58  
Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala  
1 5 10 15

Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe  
20 25 30

Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala  
35 40 45

Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser  
50 55 60

Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met  
65 70 75 80

Tyr Lys Cys Gln Leu Arg Lys Gly Trp Gln His Asn Arg Glu Gln  
85 90 95

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala  
100 105 110

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys  
115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe  
130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Xaa Val Ser Val Tyr  
145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr  
165 170 175  
Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu  
180 185 190  
Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser  
195 200 205  
Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile  
210 215 220  
Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn  
225 230 235 240  
Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys  
245 250 255  
Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser  
260 265 270  
Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu  
275 280 285  
Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys  
290 295 300  
Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys  
305 310 315 320  
Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu  
325 330 335  
Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro  
340 345 350  
Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys  
355 360 365  
Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr  
370 375 380  
Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser  
385 390 395 400  
Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro  
405 410 415  
Gln Met Ser

<210> 59

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: VEGF-C delta N delta CHis

<400> 59  
Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala  
1 5 10 15  
Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Thr  
20 25 30  
Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu  
35 40 45  
Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu  
50 55 60  
Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn Thr Phe  
65 70 75 80  
Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn  
85 90 95  
Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Ser Tyr Leu Ser Lys  
100 105 110  
Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro Lys Pro Val  
115 120 125  
Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu  
130 135 140  
Asp Val Tyr Arg Gln Val His Ser Ile Ile His His His His His His  
145 150 155 160